

attorney, Scott F. Yarnell, hereby states that the content of the computer readable disk copy of the Substitute Sequence Listing and the paper copy of the Substitute Sequence Listing are the same and no impermissible new matter is in the attached computer readable form or the paper copy of the Substitute Sequence Listing.

No new matter has been added by this amendment.

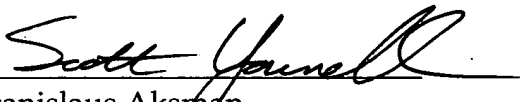
In the event any fees are incurred upon the filing of these documents, please charge the undersigned's Deposit Account No. 50-0206.

Respectfully submitted,

HUNTON & WILLIAMS

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APPENDIX A

In a specific embodiment of an artificial promoter library according to the invention for *Saccharomyces cerevisiae* said consensus sequences comprise the TATA box: TATAAA, the UAS_{GCN4p}: TGACTCA, and the TI box (SEQ IN NO:59): CTCTTAAGTGCAAGTGACTGCGA, which also functions as the binding site for the arginine repressor, argR.

When these additional motives are included, one arrives at the following 53 nucleobase degenerated sequence for an efficient promoter in *L. lactis*. Out of these 53 nucleobases, 34 bases are conserved, two are semi-conserved (R and W) and 17 are allowed to vary randomly between the four nucleobases, SEQ ID NO:60:[.]

This example illustrates the development of a temperature regulated promoter library for *L. lactis*. A regulatory element comprising an eight basepair inverted repeat that has been shown to be involved in the heatshock response of *L. lactis* is inserted a few base pairs upstream of the -35 sequence. The minimal extent of such a regulatory element seems to be 27 basepairs, SEQ ID NO:61:

When these sequences are combined, one arrives at the following 73 bp consensus sequence for a temperature regulated promoter in *L. lactis*. Out of these 73 bp, 45 are conserved, two are semi-conserved (R and W) and 26 are allowed to vary randomly between the four nucleobases, SEQ ID NO:62:[.]

APPENDIX B

24. (Once Amended) An artificial promoter library according to claim 23, wherein said consensus sequences comprise the TATA box: TATAAA, the UAS_{G_{CN}4p}: TGACTCA, and the TI box (SEQ ID NO:59): CTCTTAAGTGCAAGTGACTGCCGA, which also functions as the binding site for the arginine repressor, argR.

53. (Once Amended) A method according to claim 52, wherein said consensus sequences comprise the TATA box: TATAAA, the the UAS_{G_{CN}4p}: TGACTCA, and the TI box (SEQ ID NO:59): CTCTTAAGTGCAAGTGACTGCCGA, which also functions as the binding site for the arginine repressor, argR.